

Figure 1A
TR-11

6503184

1	GCACTTCACCTGGGTCGGGATTCTCAGGTATGAACGGTCCCAGCCACCTCCGGGCAGGG	60
61	CGGGTGAGGACGGGACGGGGCGTCCAACTGGCTGTGGCTCTTGAACCCGAGCATG	120
1	<u>M</u>	1
121	GCACAGCACGGGGCATGGGCCGTTGGGCCCTGTGCGGCCCTGGCGCTGCTGTGCGCG	180
2	<u>A O H G A M G A F R A L C G L A L L C A</u>	21
181	CTCAGCCTGGGTAGCGCCCCACCGGGGTCGGGCCCTGGCGCCTCCGTGCT	240
22	<u>L S L G Q R P T G G P G C G P G R L L L</u>	41
241	GGGACGGAACGGACGCGCGCTGCTGCCGGTTACACGACGCGCTGCTGCCGCGATTAC	300
42	<u>G T G T D A R C C R V H T T R C C R D Y</u>	61
301	CCGGGCGAGGAGTGTGTTCCGAGTGGGACTGCATGTGTCCAGCCTGAATTCCACTGC	360
62	<u>P G E E C C S E W D C M C V Q P E F H C</u>	81
<i>CD-II</i>		
361	GGAGACCCCTGCTGACGACCTGCCGGACCACCCCTGTCAGGGCAGGGCAGGGGTACAG	420
82	<u>G D P C C T T C R H H P C P P G Q G V Q</u>	101
<i>CD-III</i>		
421	TCCCAGGGAAATTCACTGGCTTCCAGTGTATCGACTGTGCCCTGGGACCTCTCC	480
102	<u>S Q G K F S F G F Q C I D C A S G T F S</u>	121
<i>CD-IV</i>		
481	GGGGGCCACGAAGGCCACTGCAAACCTGGACAGACTGCACCCAGTTGGGTTCTCACT	540
122	<u>G G H E G H C K P W T D C T Q F G F L T</u>	141
<i>CD-V</i>		
541	GTGTTCCCTGGGAACAAGACCCACAACGCTGTGCGCTCCAGGGTCCCCGCCAGAG	600
142	<u>V F P G N K T H N A V C V P G S P P A E</u>	161
<i>CD-VI</i>		
601	CCGCTTGGGTGGCTGACCGTCGTCCCTCCGTGGCGCTGCGTCCTCCCTGACC	660
162	<u>P L G W L T V V L L A V A A C V L L L T</u>	181
<i>CD-VII</i>		
661	TCGGCCCAGCTGGACTGCACATCTGGCAGCTGAGGAAGACCCAGCTGCTGGAGGTG	720
182	<u>S A Q L G L H I W Q L R K T Q L L L E V</u>	201
<i>CD-VIII</i>		
721	CCGCCGTCGACCGAACAGGCCAGAACGCTGCCAGTTCCCCGAGGAAGAGCGGGCGAGCGA	780
202	<u>P P S T E D A R S C Q F P E E E R G E R</u>	221
<i>CD-IX</i>		
781	TCGGCAGAGGAGAACGGGGCTGGAGACCTGTGGGTGTGAGCCTGCCGTCCCTCCGGG	840
222	<u>S A E E K G R L G D L W V</u>	234
<i>CD-X</i>		
841	GCCACCGACCCAGCCAGCCCCCTCCCCAGGAGCTCCCCAGGCCAGGGCTCTGCCGTC	900

Figure 1B
TR-11

901 TGCTCTGGGCCGGCCCTGCTCCCTGGCAGCAGAAGTGGGTGCAGGAAGGTGGCAGTGA 960

961 CCAGCGCCCTGGACCATGCAGTT 983

Figure 2A
TR-11SV1

1	GTGACCCACGCGTCCGGGGGCCACCCCTGGGTCCCTGCAGGGCAGCTCCTGGTGCAT	60
61	ATGGAGTTAGCACCTGGGCAGGGCAGCTGTGGGCGCAAAGGGGAGTAGCCAGGCCAC	120
121	ATGGCCCAGGAGAAAGAGACACGCTGGATAAACCCAGGTCCAGACTCCCAGCCAGGAGCC	180
1	M A P G E R D S W I N P G P D S Q P G A	20
181	CTCTGCTCCCTGGAGCCAATGTGGTGGAGAACGGACAACCTCACTCCCTGGAGGGCC	240
21	L C S L E P T V G G E R T T S L P W R A	40
241	GAGGGGAGGCCTGGGGAGGAGGGGGCTCAGCCCAGCTGCTGGGGGCTGGCCTGTCTCC	300
41	E G R P G E E G A S A Q L L G G W P V S	60
	<i>CD-I</i>	
301	TGCCAGGCGAGGAGTGCTGTCGAGTGGACTGCATGTGTGTCAGCCTGAATTCAC	360
61	C P G E E C C S E W D C M C V Q P E F H	80
	<i>CD-II</i>	
361	TGCGGAGACCCCTGCTGCACGACCTGCCGGACCACCCCTGTCCCCCAGGCCAGGGGTA	420
81	C G D P C C T T C R H H P C P P G Q G V	100
	<i>CD-II</i>	
	<i>CD-III</i>	
421	CAGTCCCAGGGAAATTCAAGTTGGCTTCCAGTGTATCGACTGTGCCTGGGACCTTC	480
101	Q S Q G K F S F G F Q C I D C A S G T F	120
	<i>CD-IV</i>	
481	TCCGGGGCCACGAAGCCACTGCAACCTTGGACAGACTGCACCCAGTCGGTTCTC	540
121	S G G H E G H C K P W T D C T Q F G F L	140
	<i>CD-V</i>	
	#	
541	ACTGTGTTCCCTGGAAACAAGACCCACAACGCTGTGCGTCCCAGGGTCCCCGGCA	600
141	T V F P G N K T H N A V C V P G S P P A	160
	<i>CD-VI</i>	
601	GAGCCGCTTGGTGCTGACCGTCGTCCCTGGCCGTGCCGCCCTGCGTCCTCCCTG	660
161	E P L G W L T V V L L A V A A C V L L L	180
	<i>CD-VII</i>	
661	ACCTCGGCCAGCTGGACTGCACATCTGGCAGCTGAGGAGTCAGTGCATGTGGCCCCGA	720
181	T S A Q L G L H I W Q L R S Q C M W P R	200
	<i>CD-VII</i>	
	<i>CD-VIII</i>	
721	GAGACCCAGCTGCTGGAGGTGCCGCCGTCGACCGAACGCCAGAGCTGCCAGTTC	780
201	E T Q L L L E V P P S T E D A R S C Q F	220
	<i>CD-VIII</i>	
	<i>CD-IX</i>	
781	CCCGAGGAAGAGCGGGCGAGCGATCGCAGAGGAGAACGGGGCGCTGGGAGACCTGTGG	840
221	P E E E R G E R S A E E K G R L G D L W	240
	<i>CD-X</i>	
841	GTGTGAGCCTGGCCGTCCCTGGGGCCACCGACCGCAGCCAGCCCCCTCCCCAGGAGCTCC	900
241	V	241

Figure 2B
TR-11SV1

901 CCAGGCCGCAGGGCTCTGCCGTCCTGCTCTGGCCGGCCCTGCTCCCTGGCAGCAGAA 960

961 GTGGGTGCAGGAAGGTGGCAGTGACCAGGCCCTGGACCATGCAGTT 1007

Figure 3A
TR-11SV2

1	ATGGGCCGTTTCGGGCCCTGTGCGGCCCTGGCGCTGCTGTGCGCGCTAGCCTGGTCAG	60
1	<u>M G A F R A L C G L A L L C A L S L G Q</u>	20
61	CGCCCCACCGGGGCTCCGGGTGCGGCCCTGGCGCTCCTGCTTGGACGGAACGGAC	120
21	<u>R P T G G P G C G P G R L L L G T G T D</u>	40
121	GCGCGCTGCTGCCGGGTTCACACGACGCGCTGCTGCCGCGATTACCCGGCCCAGCTGCTG	180
41	<u>A R C C R V H T T R C C R D Y P A Q L L</u>	60
	<i>CD-I</i>	
181	GGGGCTGGCTGTCTCCGTGCCAGGGGAGGGAGTGCTGTCCGAGTGGACTGCATGTGT	240
61	<u>G G W P V S C P G E E C C S E W D C M C</u>	80
	<i>CD-II</i>	
241	GTCCAGCCTGAATTCCACTGCGGAGACCCCTGCTGCACGACCTGCCGGCACCACCTTGT	300
81	<u>V Q P E F H C G D P C C T T C R H H P C</u>	100
	<i>CD-II</i>	<i>CD-III</i>
301	CCCCCAGGCCAGGGGTACAGTCCCAGGGAAATTCACTTGGCTTCCAGTGTATCGAC	360
101	<u>P P G Q G V Q S Q G K F S F G F Q C I D</u>	120
	<i>CD-IV</i>	
361	TGTGCCCTGGGGACCTTCTCCGGGGGCCACGAAGGCCACTGCAAACCTTGGACAGACTGC	420
121	<u>C A S G T F S G G H E G H C K P W T D C</u>	140
	<i>CD-IV</i>	<i>CD-V</i>
	#	
421	ACCCAGTTCGGTTCTCACTGTGTTCCCTGGAAACAAGACCCACAACGCTGTGCGTC	480
141	<u>T Q F G F L T V F P G N K T H N A V C V</u>	160
	<i>CD-VI</i>	
481	CCAGGGTCCCCGCCAGAGCCCTGGTGGCTGACCGTCGTCCCTGGCCGTGGCC	540
161	<u>P G S P P A E P L G W L T V V L L A V A</u>	180
	<i>CD-VI</i>	
541	GCCTGCCCTCCCTGACCTCGGCCAGCTTGGACTGCACATCTGGCAGCTGAGGAAG	600
181	<u>A C V L L L T S A Q L G L H I W Q L R K</u>	200
	<i>CD-VII</i>	
601	ACCCAGCTGCTGGAGGTGCCGCCGTCACCGAAGACGCCAGAAGCTGCCAGTCCCC	660
201	<u>T Q L L L E V P P S T E D A R S C Q F P</u>	220
	<i>CD-IX</i>	
661	GAGGAAGAGCGGGCGAGCGATCGGCAGAGGAGAAGGGGGCGCTGGAGACCTGTGGTG	720
221	<u>E E E R G E R S A E E K G R L G D L W V</u>	240
	<i>CD-X</i>	
721	TGAGCCTGGCGTCCCTGGGGCCACCGACCGCAGCCAGCCCTCCCCAGGAGCTCCCCA	780
781	GGCCGCAGGGCTCTGGTCTGCTCTGGCGGGCCCTGCTCCCCCTGGCAGCAGAAGTG	840
841	GGTGCAGGAAGGTGGCAGTGACCAGCGCCCTGGACCATGCAGTTGGCGCCGGCTGG	900

Figure 3B
TR-11SV2

901 GCCCTGCAGGAGGGAGAGAGACACAGTCATGGCCCCCTTCCTCCCTTGCTGGCCCTGA 960
961 TGGGGTGGGTCTTAGGACGGGAGGCTGTGTCGGTGTGCAGTGCCCCAGCACGGGAC 1020
1021 CCCGGCTGCAGGGACCTCAATAAACACTTGTCAGTAAAAAAAAAAAAAAA 1074

10 M - - - - - G A W A M L Y G V S M L C V L D L G Q P S V V E E P G C G P G K V Q N G S G N N T R C mGTR.aa
 1 M A Q H G A M G A F R A I L C G G L A L L C A L S L G Q R P T - G G P G C G P G R L L E G T G T D A R C TR11.aa
 1 M A P - G E R D S W - - - - - I N P G P D S Q - P G A L C S L E P T V G G E R T T S L P TR11SV1.aa
 1 M - - - - - G A F R A I L C G G L A L L C A L S L G Q R P T - G G P G C G P G R L L L G T G T D A R C TR11SV2.aa

20
 30
 40
 50

60 C S L Y A - - - - - - - - - - P G K E D C P K E B C I C V T P E Y H C C G D P Q C K mGTR.aa
 50 C R V H T T R C C R D Y P - - - - - - - - - - G E E C C S E W D C M C V Q P E F H C G D P C C T TR11.aa
 38 W R A E G R P G E E G A S A Q L L G G W P V S C P G E E C C S E W D C M C V Q P E F H C G D P C C T TR11SV1.aa
 44 C R V H T T R C C R D Y P A Q L L G G W P V S C P G E E C C S E W D C M C V Q P E F H C G D P C C T TR11SV2.aa

70
 80
 90
 100

110 I C K H Y P C Q P G Q R V E S Q G D I V F G F R C V A C A M G T F S A G R D G H C R L W T N C S Q F mGTR.aa
 76 T C R H H P C P P G Q G V Q S Q G K F S F G F Q C I D C A S G T F S G G H E G H C K P W T D C T Q F TR11.aa
 88 T C R H H P C P P G Q G V Q S Q G K F S F G F Q C I D C A S G T F S G G H E G H C K P W T D C T Q F TR11SV1.aa
 88 T C R H H P C P P G Q G V Q S Q G K F S F G F Q C I D C A S G T F S G G H E G H C K P W T D C T Q F TR11SV2.aa

120
 130
 140
 150

160 G F L T M F P G N K T H N A V C I P E P L P T E Q Y G H L T V I F L V M A A C I F E L T T V Q L G L mGTR.aa
 126 G F L T V F P G N K T H N A V C V P G S P P A E P L G W L T V V L L A V A A C V L L T S A Q L G L TR11.aa
 138 G F L T V F P G N K T H N A V C V P G S P P A E P L G W L T V V L L A V A A C V L L T S A Q L G L TR11SV1.aa
 138 G F L T V F P G N K T H N A V C V P G S P P A E P L G W L T V V L L A V A A C V L L T S A Q L G L TR11SV2.aa
 94
 170
 180
 190
 200

Figure 4A

176	H I W Q L R R Q H M C P R E T Q P F A E V Q L S A E D A C S F Q F P E E E R G E Q T - E E K C H L G	mgTR.aa
188	H I W Q L R K - - - - - T Q L L E V P P S T E D A R S C Q F P E E E R G E R S A E E K G R L G	TR11.aa
188	H I W Q L R S Q C M W P R E T Q L L E V P P S T E D A R S C Q F P E E E R G E R S A E E K G R L G	TR11SV1.aa
194	H I W Q L R K - - - - - T Q L L E V P P S T E D A R S C Q F P E E E R G E R S A E E K G R L G	TR11SV2.aa
225	G R W P	
231	D L W V	
238	D L W V	
237	D L W V	

Decoration 'Decoration #1': Shade (with solid black) residues that differ from TR11.aa.

Figure 4B

Figure 5
TR-11 Polypeptide Analysis

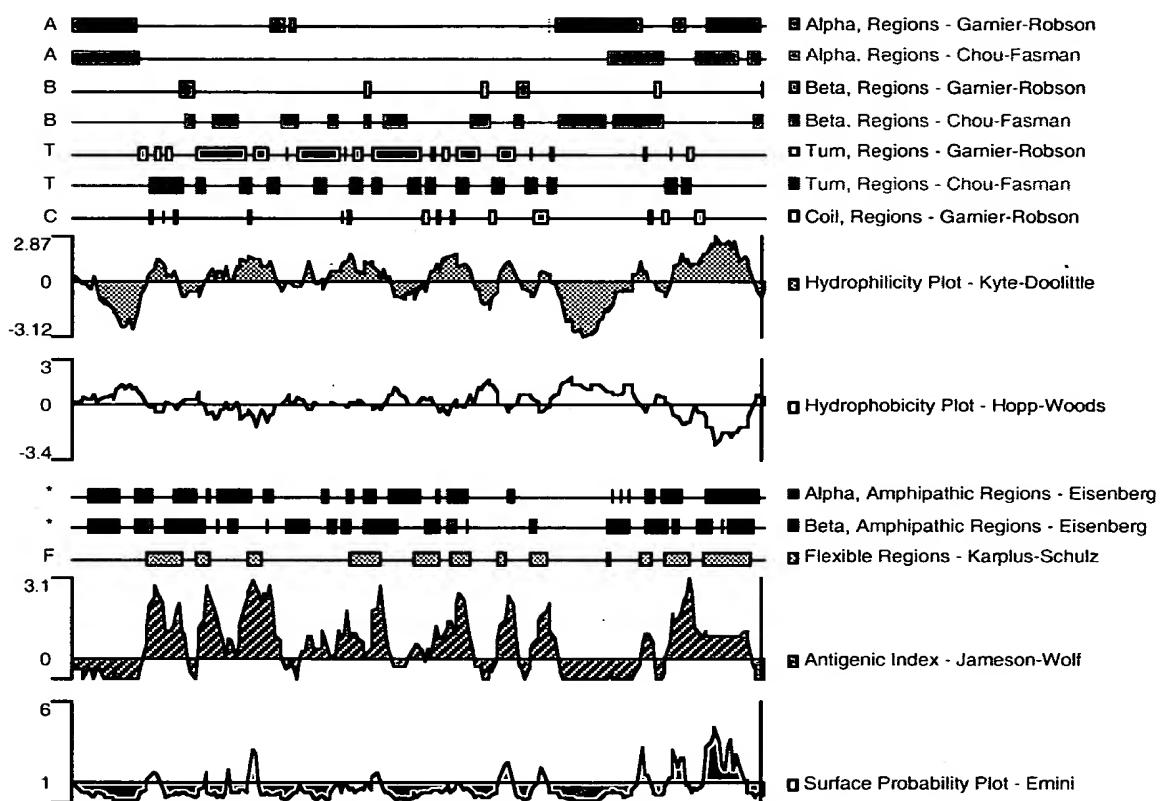


Figure 6
TR-11SV1 Polypeptide Analysis

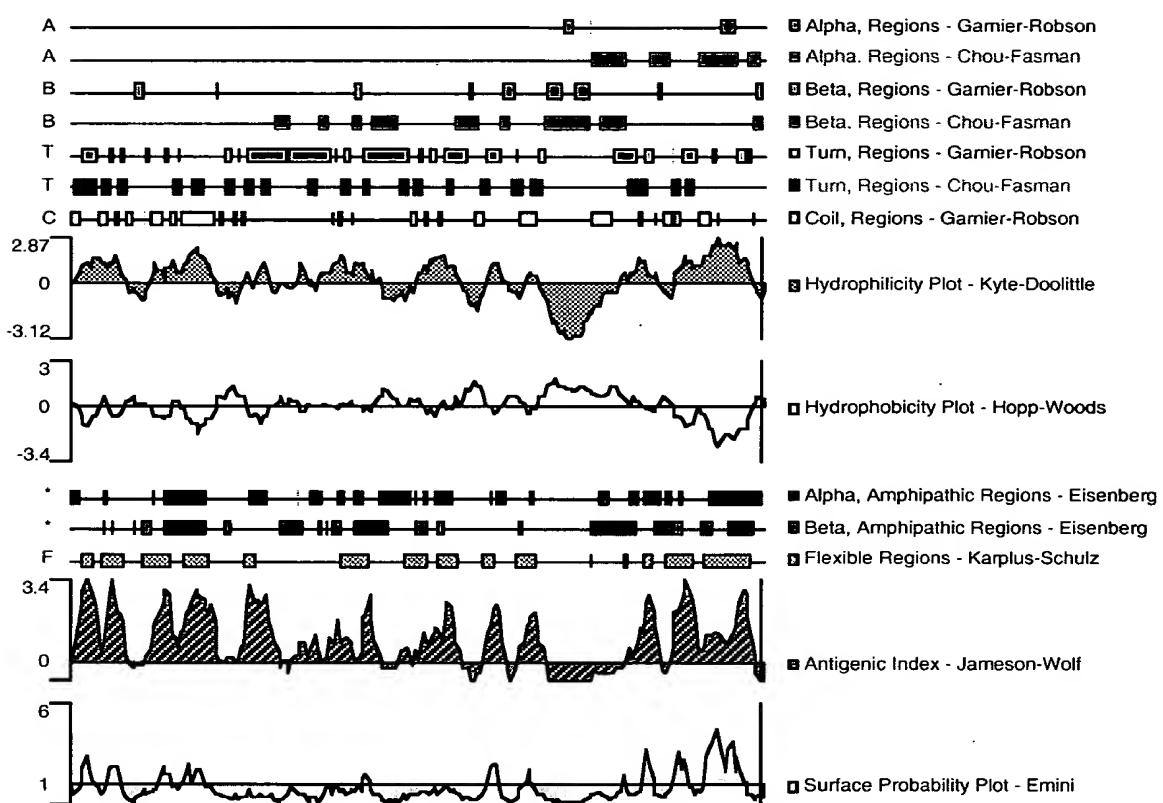


Figure 7
TR-11SV2 Polypeptide Analysis

